FIG. 1A

```
cagggatcag ggttccagga actcaggatc tgcagtgagg accagacacc actgattgca 60

gga atg tgt tcc ctc ccc atg gca aga tac tac ata att aaa tat gca   108
    Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys Tyr Ala
      1               5                  10                  15

gac cag aag gct cta tac aca aga gat ggc cag ctg ctg gtg gga gat   156
Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly Asp
                 20                  25                  30

cct gtt gca gac aac tgc tgt gca gag aag atc tgc aca ctt cct aac   204
Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Thr Leu Pro Asn
             35                  40                  45

aga ggc ttg gac cgc acc aag gtc ccc att ttc ctg ggg atc cag gga   252
Arg Gly Leu Asp Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly
         50                  55                  60

ggg agc cgc tgc ctg gca tgt gtg gag aca gaa gag ggg cct tcc cta   300
Gly Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser Leu
     65                  70                  75

cag ctg gag gat gtg aac att gag gaa ctg tac aaa ggt ggt gaa gag   348
Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu
 80                  85                  90                  95

gcc aca cgc ttc acc ttc ttc cag agc agc tca ggc tcc gcc ttc agg   396
Ala Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg
                100                 105                 110

ctt gag gct gct gcc tgg cct ggc tgg ttc ctg tgt ggc ccg gca gag   444
Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu
            115                 120                 125

ccc cag cag cca gta cag ctc acc aag gag agt gag ccc tca gcc cgt   492
Pro Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Ala Arg
        130                 135                 140

acc aag ttt tac ttt gaa cag agc tgg tag ggagacagga aactgcgttt     542
Thr Lys Phe Tyr Phe Glu Gln Ser Trp
    145                 150

tagccttgtg cccccaaacc aagctcatcc tgctcagggt ctatggtagg cagaataatg 602

tcccccgaaa tatgtccaca tcctaatccc aagatctgtg catatgttac catacatgtc 662

caaagaggtt ttgcaaatgt gattatgtta aggatcttga aatgaggaga caatcctggg 722

ttatccttgt gggctcagtt taatcacaag aaggaggcag gaagggagag tcagagagag 782

aatggaagat accatgcttc taattttgaa gatggagtga ggggccttga gccaacaaat 842

gcaggtgttt ttagaaggtg gaaaagccaa gggaacggat tctcctctag agtctccgga 902
```

FIG. 1B

aggaacacag ctcttgacac atggatttca gctcagtgac acccatttca gacttctgac 962

ctccacaact ataaaataat aaacttgtgt tattgtaaac ctctaaaaaa aaaaaaaa 1020

FIG. 2A

```
cagggatcag ggttccagga actcaggatc tgcagtgagg accagacacc actgattgca 60

gga atg tgt tcc ctc ccc atg gca aga tac tac ata att aaa tat gca   108
    Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys Tyr Ala
      1               5                  10                  15

gac cag aag gct cta tac aca aga gat ggc cag ctg ctg gtg gga gat   156
Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly Asp
                 20                  25                  30

cct gtt gca gac aac tgc tgt gca gag aag atc tgc ata ctt cct aac   204
Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Ile Leu Pro Asn
             35                  40                  45

aga ggc ttg gcc cgc acc aag gtc ccc att ttc ctg ggg atc cag gga   252
Arg Gly Leu Ala Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly
         50                  55                  60

ggg agc cgc tgc ctg gca tgt gtg gag aca gaa gag ggg cct tcc cta   300
Gly Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser Leu
     65                  70                  75

cag ctg gag gat gtg aac att gag gaa ctg tac aaa ggt ggt gaa gag   348
Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu
 80                  85                  90                  95

gcc aca cgc ttc acc ttc ttc cag agc agc tca ggc tcc gcc ttc agg   396
Ala Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg
                100                 105                 110

ctt gag gct gct gcc tgg cct ggc tgg ttc ctg tgt ggc ccg gca gag   444
Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu
            115                 120                 125

ccc cag cag cca gta cag ctc acc aag gag agt gag ccc tca gcc cgt   492
Pro Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Ala Arg
        130                 135                 140

acc aag ttt tac ttt gaa cag agc tgg tag ggagacagga aactgcgttt     542
Thr Lys Phe Tyr Phe Glu Gln Ser Trp
    145                 150

tagccttgtg cccccaaacc aagctcatcc tgctcagggt ctatggtagg cagaataatg 602

tccccccgaaa tatgtccaca tcctaatccc aagatctgtg catatgttac catacatgtc 662

caaagaggtt ttgcaaatgt gattatgtta aggatcttga aatgaggaga caatcctggg 722

ttatccttgt gggctcagtt taatcacaag aaggaggcag gaagggagag tcagagagag 782

aatggaagat accatgcttc taattttgaa gatggagtga ggggccttga gccaacaaat 842

gcaggtgttt ttagaaggtg gaaaagccaa gggaacggat tctcctctag agtctccgga 902
```

FIG. 2B

aggaacacag ctcttgacac atggatttca gctcagtgac acccatttca gacttctgac 962

ctccacaact ataaaataat aaacttgtgt tattgtaaac ctctaaaaaa aaaaaaaa 1020

FIG. 3

```
gctcccgcca ggagaaagga acattctgag gggagtctac accctgtgga gctcaag     57

atg gtc ctg agt ggg gcg ctg tgc ttc cgt gag gac cag aca cca ctg   105
Met Val Leu Ser Gly Ala Leu Cys Phe Arg Glu Asp Gln Thr Pro Leu
  1               5                  10                  15

att gca gga atg tgt tcc ctc ccc atg gca aga tac tac ata att aaa   153
Ile Ala Gly Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys
             20                  25                  30

tat gca gac cag aag gct cta tac aca aga gat ggc cag ctg ctg gtg   201
Tyr Ala Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val
         35                  40                  45

gga gat cct gtt gca gac aac tgc tgt gca gag aag atc tgc ata ctt   249
Gly Asp Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Ile Leu
     50                  55                  60

cct aac aga ggc ttg gcc cgc acc aag gtc ccc att ttc ctg ggg atc   297
Pro Asn Arg Gly Leu Ala Arg Thr Lys Val Pro Ile Phe Leu Gly Ile
 65                  70                  75                  80

cag gga ggg agc cgc tgc ctg gca tgt gtg gag aca gaa gag ggg cct   345
Gln Gly Gly Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro
                 85                  90                  95

tcc cta cag ctg gag gat gtg aac att gag gaa ctg tac aaa ggt ggt   393
Ser Leu Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly
            100                 105                 110

gaa gag gcc aca cgc ttc acc ttc ttc cag agc agc tca ggc tcc gcc   441
Glu Glu Ala Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala
        115                 120                 125

ttc agg ctt gag gct gct gcc tgg cct ggc tgg ttc ctg tgt ggc ccg   489
Phe Arg Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro
    130                 135                 140

gca gag ccc cag cag cca gta cag ctc acc aag gag agt gag ccc tca   537
Ala Glu Pro Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser
145                 150                 155                 160

gcc cgt acc aag ttt tac ttt gaa cag agc tgg tag ggagacagga        583
Ala Arg Thr Lys Phe Tyr Phe Glu Gln Ser Trp
                165                 170

aactgcgttt tagccttgtg cccccaaacc aagctcatcc tgctcagggt ctatggtagg 643

cagaataatg tcccccgaaa tatgtccaca tcctaatccc aagatctgtg catatgttac 703

catacatgtc caaagaggtt ttgcaaatgt gattatgtta a                     744
```

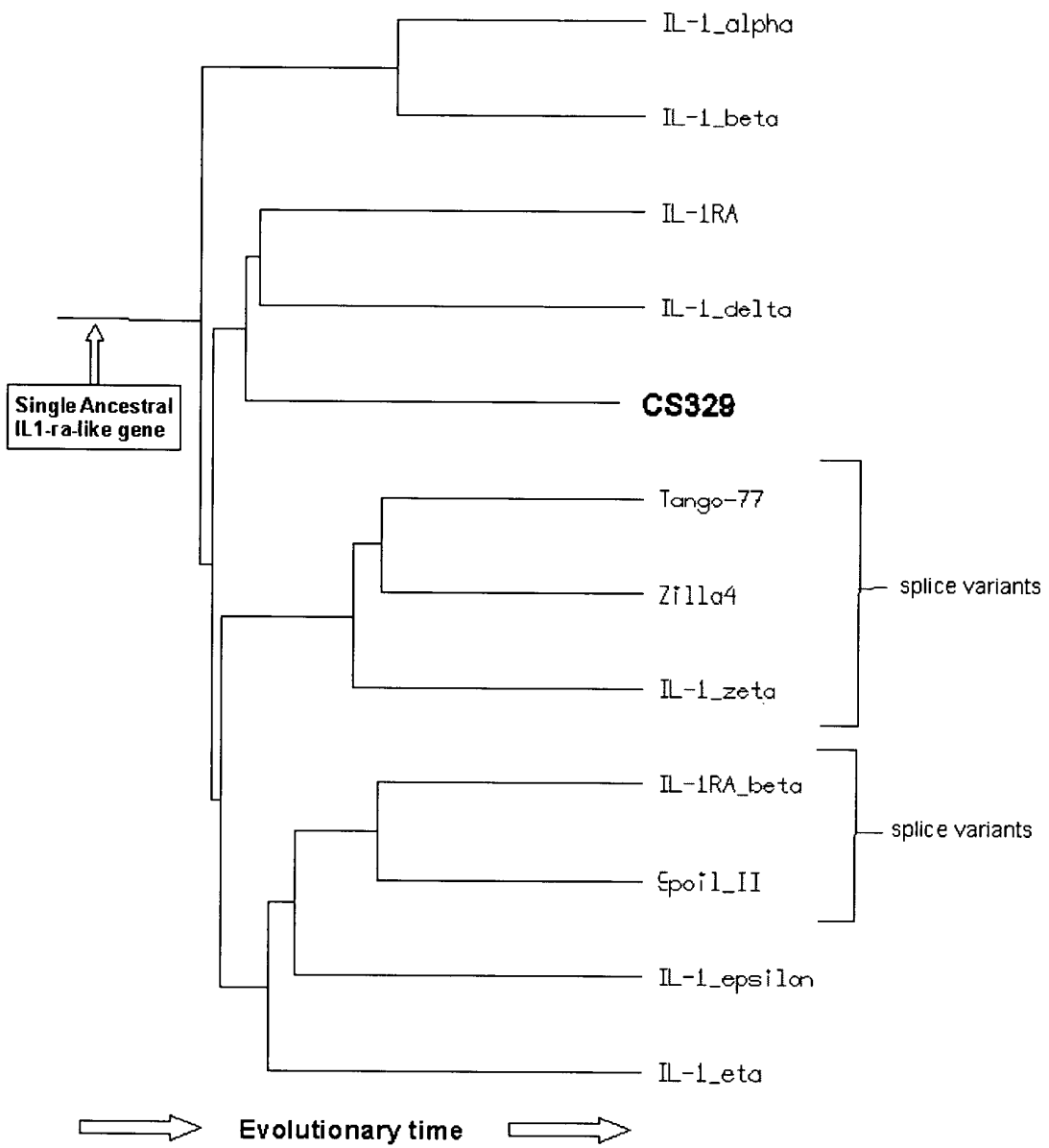
FIG. 4A

```
                1                                                    50
  IL-1_alpha MAEVPKLASE MMAYYSGNED DLFFEADGPK QMKCSFQDLD LCPLDGGIQL
   IL-1_beta ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      IL-1RA ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  IL-1_delta ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       CS329 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    Tango-77 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      Zilla4 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   IL-1_zeta ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
 IL-1RA_beta ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    Spoil_II ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
IL-1_epsilon ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    IL-1_eta ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~

                51                                                   100
  IL-1_alpha RISDHHYSKG FRQAASVVVA MDKLRKMLVP CPQTFQENDL STFFPFIFEE
   IL-1_beta ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      IL-1RA ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~MEIC RGLRSHLITL
  IL-1_delta ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       CS329 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    Tango-77 ~~~~~~~~~~ ~~MSFVGENS GVKMGSEDWE KDEPQCCLED PAGSPLEPGP
      Zilla4 ~~~~~~~~~~ ~~MSFVGENS GVKMGSEDWE KDEPQCCLED PAGSPLEPGP
   IL-1_zeta ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ MSGCDRRETE
 IL-1RA_beta ~~~~~~~~~~ MRGTPGDADG GGRAVYQS.. .......... ..........
    Spoil_II ~~~~~~~~~~ MRGTPGDADG GGRAVYQSSE SNAVGMGLWR LRPSALTLSP
IL-1_epsilon ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    IL-1_eta ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~

                101                                                  150
  IL-1_alpha EPIFFDTWDN EAYVHDAPVR SLNCTLRDSQ QKSLVMSGPY ELKALHLQGQ
   IL-1_beta ~~~~~~~~~~ ~~~~~~APVR SLNCTLRDSQ QKSLVMSGPY ELKALHLQGQ
      IL-1RA LLFLFHSETI CRPSGRKSSK IQAFRIWDVN QKTFYLRNN. QLVAGYLQGP
  IL-1_delta ~~~~~~~~~~ ~~~~~MVLSG ALCFRMKDSA LKVLYLHNN. QLLAGGLHAG
       CS329 ~~~~~~~~~~ ~~~~MCSLPM ARYYIIKYAD QKALYTRDG. QLLVGDPVAD
    Tango-77 SLPTMNFVH. .T..... .......... .......... ..........
      Zilla4 SLPTMNFVH. .TSPKVKNLN PKKFSIHDQD HKVLVLDSG. NLIA..VPDK
   IL-1_zeta TKGKNSFKKR LRGPKVKNLN PKKFSIHDQD HKVLVLDSG. NLIA..VPDK
 IL-1RA_beta .......... .......MCK PITGTINDLN QQVWTLQGQ. NLVA..VPRS
    Spoil_II VEAPAFSAPL CTLPFPPVCK PITGTINDLN QQVWTLQGQ. NLVA..VPRS
IL-1_epsilon ~~~~~~~~~~ ~MEKALKIDT PQQGSIQDIN HRVWVLQDQ. TLIA..VPRK
    IL-1_eta ~~~~~~~~~~ ~~MNPQREAA PKSYAIRDSR QMVWVLSGN. SLIA..APLS

                151                                                  200
  IL-1_alpha DMEQQVVFSM ...SFVQGEE SNDKIPVALG LKEKNLYLSC VLKDDK..PT
   IL-1_beta DMEQQVVFSM ...SFVQGEE SNDKIPVALG LKEKNLYLSC VLKDDK..PT
      IL-1RA NVNLEEKIDV VP.....IEP ....HALFLG IHGGKMCLSC VKSGDE..TR
  IL-1_delta KVIKGEEISV VPNRWLDASL ....SPVILG VQGGSQCLSC .GVGQE..PT
       CS329 NC.CAEKICT LPNRGLDRTK ....VPIFLG IQGGSRCLAC VETEEG..PS
    Tango-77 .....KIFFA LASSLSSA.S AEKGSPILLG VSKGEFCLYC DKDKGQSHPS
      Zilla4 NYIRPEIFFA LASSLSSA.S AEKGSPILLG VSKGEFCLYC DKDKGQSHPS
   IL-1_zeta NYIRPEIFFA LASSLSSA.S AEKGSPILLG VSKGEFCLYC DKDKGQSHPS
 IL-1RA_beta DSVTPVTVAV ITCKYPEALE QGRGDPIYLG IQNPEMCLYC EKVGEQ..PT
    Spoil_II DSVTPVTVAV ITCKYPEALE QGRGDPIYLG IQNPEMCLYC EKVGEQ..PT
IL-1_epsilon DRMSPVTIAL ISCRHVETLE KDRGNPIYLG LNGLNLCLMC AKVGDQ..PT
    IL-1_eta RSIKPVTLHL IACRDTEFSD KEKGNMVYLG IKGKDLCLFC AEIQGK..PT
```

FIG. 4B

```
                201                                                  250
  IL-1_alpha LQLESVDPKN Y..PKKKMEK RFVFNKIEIN NKLEFESAQF PNWYISTSQA
   IL-1_beta LQLESVDPKN Y..PKKKMEK RFVFNKIEIN NKLEFESAQF PNWYISTSQA
      IL-1RA LQLEAVNITD LSENRKQDKR .FAFIRSDSG PTTSFESAAC PGWFLCTAME
  IL-1_delta LTLEPVNIME LYLGAKESKS .FTFYRRDMG LTSSFESAAY PGWFLCTVPE
       CS329 LQLEDVNIEE LYKGGEEATR .FTFFQSSSG SAFRLEAAAW PGWFLCGPAE
    Tango-77 LQLKKEKLMK LAAQKESARR PFIFYRAQVG SWNMLESAAH PGWFICTSCN
      Zilla4 LQLKKEKLMK LAAQKESARR PFIFYRAQVG SWNMLESAAH PGWFICTSCN
   IL-1_zeta LQLKKEKLMK LAAQKESARR PFIFYRAQVG SWNMLESAAH PGWFICTSCN
 IL-1RA_beta LQLKEQKIMD LYGQPEPV.K PFLFYRAKTG RTSTLESVAF PDWFIA.SSK
    Spoil_II LQLKEQKIMD LYGQPEPV.K PFLFYRAKTG RTSTLESVAF PDWFIA.SSK
IL-1_epsilon LQLKEKDIMD LYNQPEPV.K SFLFYHSQSG RNSTFESVAF PGWFIAVSSE
    IL-1_eta LQLKEKNIMD LYVEKKAQ.K PFLFFHNKEG STSVFQSVSY PGWFIATSTT

                251                                          290
  IL-1_alpha ENMPVFL... .GGTKGGQDI TDFTMQFVSS ~~~~~~~~~~
   IL-1_beta ENMPVFL... .GGTKGGQDI TDFTMQFVSS ~~~~~~~~~~
      IL-1RA ADQPVSLTNM PDEG...VMV TKFYFQEDE~ ~~~~~~~~~~
  IL-1_delta ADQPVRLTQL PENGGWNAPI TDFYFQQCD~ ~~~~~~~~~~
       CS329 PQQPVQLTKE SEPSAR.... TKFYFEQSW~ ~~~~~~~~~~
    Tango-77 CNEPVGVTDK FENRKH.... IEFSFQPVCK AEMSPSEVSD
      Zilla4 CNEPVGVTDK FENRKH.... IEFSFQPVCK AEMSPSEVSD
   IL-1_zeta CNEPVGVTDK FENRKH.... IEFSFQPVCK AEMSPSEVSD
 IL-1RA_beta RDQPIILTSE LGKSYN.... TAFELNIND~ ~~~~~~~~~~
    Spoil_II RDQPIILTSE LGKSYN.... TAFELNIND~ ~~~~~~~~~~
IL-1_epsilon GGCPLILTQE LGKANT.... TDFGLTMLF~ ~~~~~~~~~~
    IL-1_eta SGQPIFLTKE RGITNN.... TNFYLDSVE~ ~~~~~~~~~~
```

FIG. 5


Phylogenetic Tree of the Emerging IL1-ra Gene Family
IL-1_alpha
IL-1_beta
IL-1RA
IL-1_delta
CS329
Single Ancestral IL1-ra-like gene
Tango-77
Zilla4
IL-1_zeta
splice variants
IL-1RA_beta
Spoil_II
splice variants
IL-1_epsilon
IL-1_eta
Evolutionary time

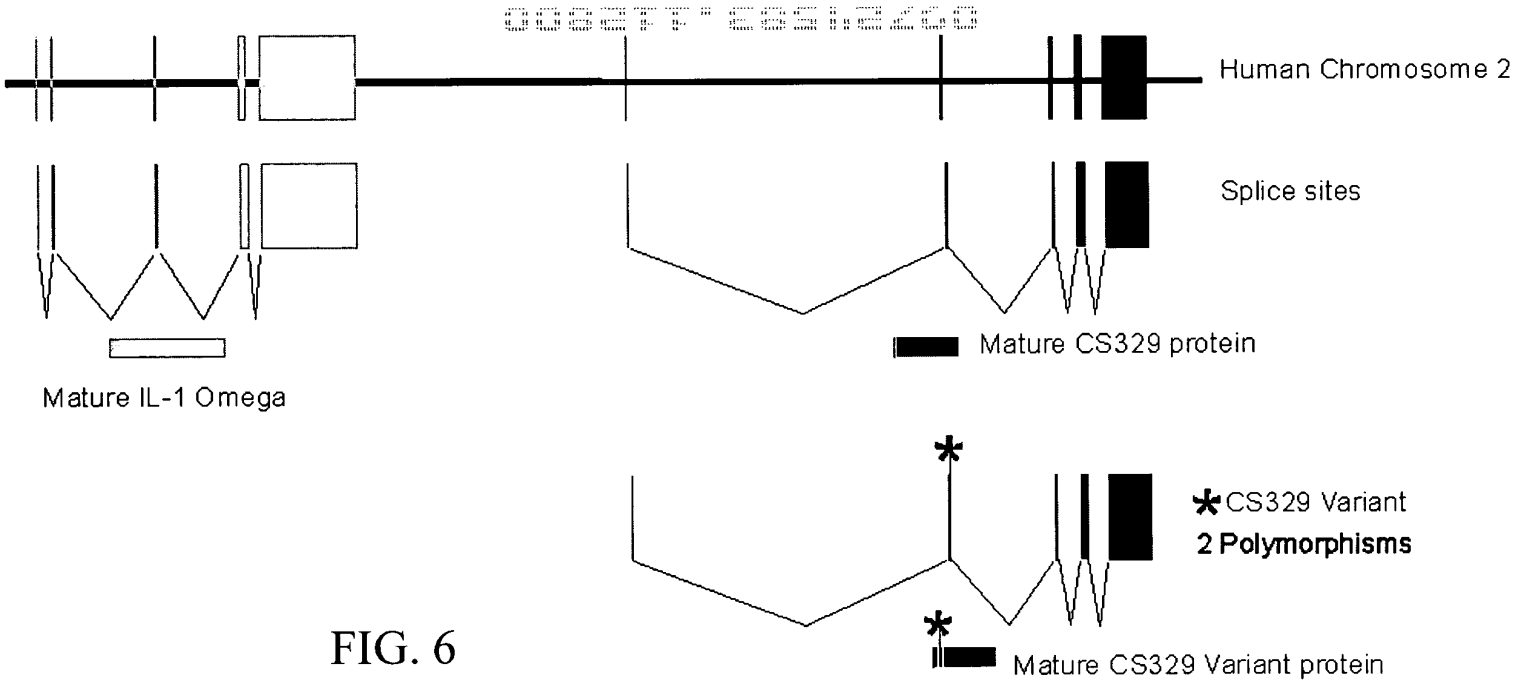

Human Chromosome 2
Splice sites
Mature CS329 protein
Mature IL-1 Omega
*CS329 Variant
2 Polymorphisms
Mature CS329 Variant protein

FIG. 6

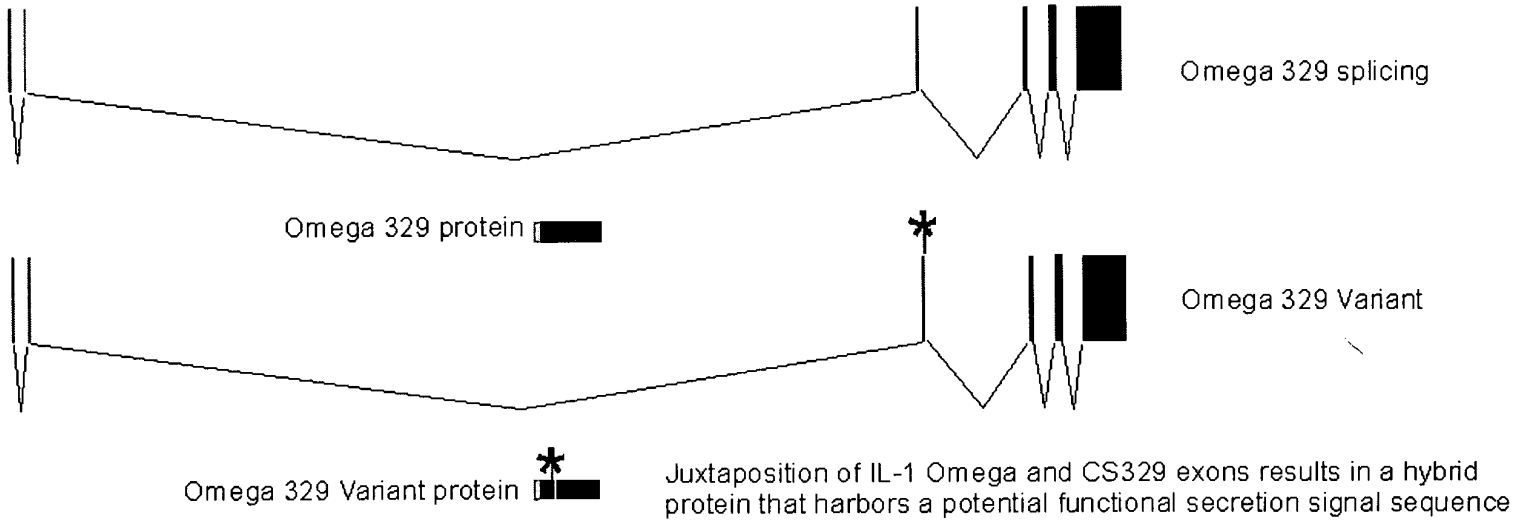

Omega 329 splicing
Omega 329 protein
Omega 329 Variant
Omega 329 Variant protein
Juxtaposition of IL-1 Omega and CS329 exons results in a hybrid protein that harbors a potential functional secretion signal sequence

FIG. 7

```
atg tgc tcc ctt ccc atg gca aga tac tac ata atc aag gat gca cat   48
Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys Asp Ala His
  1               5                  10                  15

caa aag gct ttg tac aca cgg aat ggc cag ctc ctg ctg gga gac cct   96
Gln Lys Ala Leu Tyr Thr Arg Asn Gly Gln Leu Leu Leu Gly Asp Pro
            20                  25                  30

gat tca gac aat tat agt cca gag aag gtc tgt atc ctt cct aac cga   144
Asp Ser Asp Asn Tyr Ser Pro Glu Lys Val Cys Ile Leu Pro Asn Arg
         35                  40                  45

ggc cta gac cgc tcc aag gtc ccc atc ttc ctg ggg atg cag gga gga   192
Gly Leu Asp Arg Ser Lys Val Pro Ile Phe Leu Gly Met Gln Gly Gly
     50                  55                  60

agt tgc tgc ctg gcg tgt gta aag aca aga gag gga cct ctc ctg cag   240
Ser Cys Cys Leu Ala Cys Val Lys Thr Arg Glu Gly Pro Leu Leu Gln
 65                  70                  75                  80

ctg gag gat gtg aac atc gag gac cta tac aag gga ggt gaa caa acc   288
Leu Glu Asp Val Asn Ile Glu Asp Leu Tyr Lys Gly Gly Glu Gln Thr
                85                  90                  95

acc cgt ttc acc ttt ttc cag aga agc ttg gga tct gcc ttc agg ctt   336
Thr Arg Phe Thr Phe Phe Gln Arg Ser Leu Gly Ser Ala Phe Arg Leu
            100                 105                 110

gag gct gct gcc tgc cct ggc tgg ttt ctc tgt ggc cca gct gag ccc   384
Glu Ala Ala Ala Cys Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu Pro
        115                 120                 125

cag cag cca gtg cag ctc acc aaa gag agt gaa ccc tcc acc cat act   432
Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Thr His Thr
    130                 135                 140

gaa ttc tac ttt gag atg agt cgg taa                              459
Glu Phe Tyr Phe Glu Met Ser Arg
145                 150
```

FIG. 8

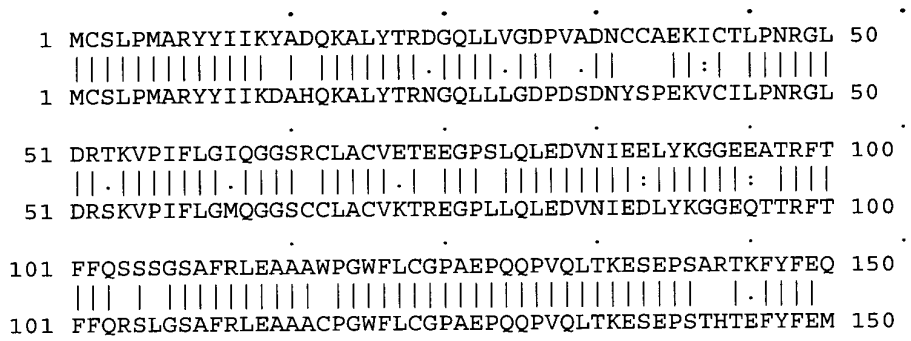

1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGL 50
1 MCSLPMARYYIIKDAHQKALYTRNGQLLLGDPDSDNYSPEKVCILPNRGL 50
51 DRTKVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFT 100
51 DRSKVPIFLGMQGGSCCLACVKTREGPLLQLEDVNIEDLYKGGEQTTRFT 100
101 FFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTKESEPSARTKFYFEQ 150
101 FFQRSLGSAFRLEAAACPGWFLCGPAEPQQPVQLTKESEPSTHTEFYFEM 150
151 SW 152
151 SR 152

FIG. 9A

```
actagtctcc catagacaac agctgaatgt acgaggtcag aagcaaggcc tgccccagaa 60
ccattgcaag ccaggtgctg tcttgattgt agcctcataa aaaactgatg cagaattgcc 120
ccaccaacat gctccagatt cctgctccac agaaaccctg tgaactaacc atgttgcttt 180
tagattctgc agtaagttga taatctgcag taaataacat tcgatgaaag agaaacatgt 240
gtagttactt tattatgatc aaaactttat ttctccactc tttccatttt ccttctcaga 300
attgacacca gcctttcact aacccaaata gcctatttaa atgctgatca tacttctctt 360
gttaactgtt acctgttccc aaaaggtaca attccctttc gaccatagct gcatctccca 420
cctgcacacc aggatgtttc tcatatttct acctaaaaca ttggggacta caagtgaaag 480
caaaagaggg ggtccatatc agaaccccag gtatttagct gtaaaactca cttgtcaggc 540
cagcttgaca ggtttacagt ttgtagaagg accagaaaga aggtagccaa gacagaagag 600
gcaacctctg cttgtcctag aaccttcagt ccatatacat ctaagctccc cagcaccatt 660
tctaccacag acctctcaga gttcctgagg atgcagaccc caggacactg acctcagttt 720
ccaggcaggg tttctgcaca ccccccttcac actgcctgac tgggagttag tctcatggtg 780
caacactact ttgggacact gtacccatcc cctcgaccta cagaaaccat tcacttttca 840
aggtcacctc ctataggaag tatttgaaaa gatgagagtc atggtcattt gctatgataa 900
tattctgtgc ttatctccct gtaaaaagtt ggcttggggt ctctggcatg catctgacct 960
taaggttgga gctgcaccaa tatgttttta agcacccggc ataatgcttc gcaaaatttc 1020
agaacatggt ttgtacagaa tgtactttcc tccactcata caaacccttg taaaagagta 1080
gtttgaatcc caactcattc ttgaaggcca ccttttgtag ggtgacagaa tttaaaaata 1140
cagaatttaa aaatacttta tcccagggaa gctcacactt ctaaatccag aatgaaagaa 1200
gaaatagaaa cacacttgtg gtggcggtgg tggtggtgat ggtggtcgtg gtggtggtgg 1260
tggtggtggt ggtgatggtg gtggtggtgg tggtggtggt ggtcgtggtg gtgtaatgat 1320
cacagtaaag tgaggcatca tggcctgaga gagtcaggca tcacagctat tcaagtgaaa 1380
actacctact actgatttta gagttctata attttagtag cagccacagg cctggggcct 1440
gggcctatat tttcagagag gaaatgttca cagcaggtca actgcagaca gtgaagatca 1500
gaaatgtttc ataatcaggt catcagagaa aaggcaaagg agctgatgga ctttatcctg 1560
aaaaagcaaa atccaaccca cctcatgctt aatgcattca aaggtctgcg ggcagaagaa 1620
```

FIG. 9B

tacattttgc tttttattat tataaattac ctggagaata tttttgtctg aattatctcc 1680

caaatattaa ccataaaaat aaaaaattcc atgtgtgctt ctcccagggg ctataaagcc 1740

cctggtctta gagttgttgg ggcaaaacct gacctttgaa gtagttactt ttgaagatgc 1800

cataccatac atttggccac ttggagagag tctaatgtca catctaaagg gttactctga 1860

tgctctgttt tctcatatgc ccttggctta cagctaacta tggctccagc taaactataa 1920

agttccttgg caacagagat ggtacgctat gtgtctttga cacagcagaa taaatgctta 1980

gtgaacatta ctgattgcct gacaggacac ctcacacttt ggtactttca acagagggat 2040

gtaaacttat gaagaacaat gaagaatgaa tattggcaat aaaagcaaaa attggttaac 2100

ccaattctag ctctgaaatc atttttaggt agtgggaagt ctttttgttt tgtttattca 2160

ctttacatcc caattgctgt cctccctcca agttccccac caccaccaca gtccttttc 2220

cctccccttc tcctctgaga gaatggagaa ccctcctgga tattccccca tcatgaaaca 2280

ttaagtctct gcagggctag acacttcccc cagtgaggcc agtcagggca gcccagctag 2340

aaaaagcata tcccacagac agacaacagc ttttgggata gccccgttcc agttgtttag 2400

gatccacatg aaggctgagc tgcacatctg ctacatatga atgaggaggc ctaggtccag 2460

cctgtgtatg ttctttggtt ggtggttcag actctgagag ccccaagggt ccaggtcagt 2520

tgactctgtt ggtcttcctg tggacaccct gtccccttcc agcccacaat ccttccccta 2580

atccttctcc ttctcacttc cataagagtg tgaggagtct ttaaaaacat gaagcatttt 2640

atctccccag ggcaacacat ggaaatgaaa gattgtgaaa agtaatttaa agaaaaagaa 2700

aaaaaaattt aacaaggaat aagaatcttg tttctctgaa aatgcttaag agtgtggaaa 2760

acataaactg gattctaata gaatgcaatt ggattgtaat gaaaacctat caaagttatg 2820

aaatagcttt cactaccttg cacaaaatct cttggcatgt gtgttgttgg caaattttct 2880

tgttagttta aaaccacaac aataacaaca aaatagcaaa aattgggtct cagcctcatt 2940

catttttct catttcttgc tctgtgatcg tctgggtctt aagctgacac ctcaccaatt 3000

cctcatcaag acctttgtgg aaatttgcaa atgtcccaaa aaggagaatt acaataagtc 3060

agagaacgtt ctgtccaatt ctttatccct agtgatggat gagtaaagga tgtataagag 3120

atggataaat ggactgatgt acagataaat gaaggaatat gtacatggtt aggtggatag 3180

atgacttact caacagatga gtagaaggat gagaaataga tggacagctg gactgaggca 3240

FIG. 9C

```
tgcaaagtca actggagaac tgagtctctt gaccatgcac tgtccagggt ctcatattcc 3300
ctagagtcca gggcccatgg ctcctgtgcc atccccatgc aaatctaagg ttaatacgtt 3360
ctacagctga gtttccttac atatgtgtct cagtaagttt gtatcaacta attaaatctg 3420
aaaggagttc cttctgatct tcccaaacag agccacactc gtgatgaagt cagccctgct 3480
tcattgtggt tctctggatg catctggctt ccatcagcat aatctttcta ttcttgatcc 3540
ttccaacctc ttcaggtctc agacagaacc ccatggagca tcaaagaggt ttgaccccag 3600
cattgtttat gtagctgcaa aaccactaat aacacagtca atgacagtag ctacagagac 3660
agcaggtcag tgtctggcct ctgtcaaggc tttatgagtg actctctccc cttcccgcaa 3720
atactcatta atctccccac ctccttatta tttggactgt gttgaagata ttatgaaatc 3780
tctgggctct tcttcccgga tctagagcca attacagatt ctgtaggttt gacccaccct 3840
gaccagacat tataaacaca gtgctggtgc cctgaagaaa acagttggag actccaggca 3900
ttagaatcca ggcaccagga actacaggtc agtggtgaca gtcggtctct ctgtgtatct 3960
cttacacaca cacacataca cacacacaac acaacataca cacacataca acacacaaca 4020
catacacata caacacatac acacacacaa cacttttctg taatgtctcc aaaattctca 4080
ggctctaggg aagaagaaat gtcttttaga gaatgcggtg tgatgttcta taagtctagg 4140
aatacttgat agaatttaat gagaagtata gattaggtca aagcaagggt actacatatt 4200
tggaaccaca gagttttgaa agtcatctca aaagaaatta tttaggccag agatgttcaa 4260
aaaatgtttt gtttgtgaca tatggaagct cccatggaga cattctgtga ttctcatcaa 4320
tagacagtag ggatgccacc aaggtgctaa cgtcttcatc accccatcat ctatcataca 4380
tccaaatggt ttctttgaaa acaatctcct tgtgaaactt aaagtagcct tgaaaatata 4440
ataatcttgt ccagcctctc atttcaatgg gaatagattg aaggcctaag gaccaaaaca 4500
aaaaacaaaa caaacaaaat aaaaacacca aaaaaaaaac ccataaaatg aatgagtagc 4560
taagttattt ttagaatcca gcctttcagt caaagcttga ttcatgcata tctgtgttct 4620
gatcttaagg tgctgtgtct gtcagttgta tagttggata gaggtacaga tgagctatat 4680
acatcatgct tcaagatttc aggatcttat aacttttata aagcaaataa tttgtcttaa 4740
tgcacactaa taaacaatat agcaaagttt gacaggagtt cagagtactg ttagagaagt 4800
gaagggaaga attttgttat gatagtaaag gggaaaatca aattttgagt catggaatca 4860
```

FIG. 9D

```
tacatagttt gacatagaaa gaaccttggc aaccacataa tctaatgcat gagcccaaga 4920
actggcctgt gtttttaaga tctcattctc agctgttatg taactgaaca gacaagatac 4980
taagcccaag tatagtgaag ccatgtccag tgatcttaat aggagtgaca ggaatggttg 5040
gtgatgaaga ggggtggatt ttgagcagga ataccaaaag caatgctgac tgtgcccttg 5100
gagagaatta gcatgagtcc ttgagagaaa aatgagatgc tattgcacaa gcaacctagg 5160
gccagatggt gtcaagatag gtggccatcg tggactttag aaccaggcag gaatgtgatc 5220
agagatgtac tttatgtagg ttaggtttga ttcagaaacc aggagggtta gcatgtttac 5280
aatggtgact aaaaacaagc acaaggttat actttaaaga aataatctct gaaaagaagg 5340
gaggtatatt ttcagtgccg gaaagaggaa tattacaaaa gtgagaggag tagatttgag 5400
aaagagaagt ggattgtgga ggagcagatg ctcaccacgc ccttacactc acttgaactg 5460
acacccaaag atgaaggtgt gctgtggact gctgaagctc agcctgtggc tgggaagcag 5520
taaacaaaat tgctcatcac agctgtacaa gatattccat agcatataaa aataaaagtg 5580
cttaggctat tctcttacaa ctctcagcct tatgaatgac ccggaaggaa aagaactcta 5640
caatgtgcct gtgtctgttc ttacttcctc tgccacaagc aaaagagcct tgggaattgg 5700
ctcagaggga acgtcatcaa acaggctggc cttgaggctg ggctgttatt cgtctacctg 5760
ggatagagga attcgctatt cttttataat ccaagtgtgg cctggggacc agcagcatta 5820
ttaagacctg gttgcatgtt tgaaatgcag tctcagattt catcccagac ctaaagagta 5880
acactgtttt catgaggata caagattaag aaatatgcat tagagagtaa ttggctaaat 5940
gggtaaatgt catgcaagca ggaggatctg attgactccc caggacccac acagttccca 6000
tgccgtagag cacatctgta atcacagtag gcgtatgatg aaatgggagg tgaatcaaga 6060
gaatctctag cagctacggg ctggccagcc tcccatgcac agcactaaat aaggcaagga 6120
ccaatacctg aagttgtccc attaccttca catatacacc acggcatgtg tgtacttgta 6180
ctcacacata caaacaaata cacacgtgca cacatacaaa actcagagat taaggacaat 6240
tggcctgaca tatcagttcc taagcctggc tcattgcttg taacactaca agcagtatta 6300
aataaggata ggcgagagaa cagttaccga atggttcaga agtggggcca tgcctgtgac 6360
tttaaacaaa tgtttcatat ttttaaataa taacacttag attacaaaat aaatttacta 6420
caggaaaatg ttaagaacta tcaacaacca ttgactatcc tgtcggccac aaatgagtgt 6480
```

FIG. 9E

tataacaagc accagccgtc cttgtccaca tgtgtgtgtg tctacacagc tatgaattta 6540

attgggataa taatgtgcac attctttacg gcctgcagtt tttacttcat gtatttgaaa 6600

tgtttgtgcc acaaatgtca tctttaagga gcatatcctt atttcctgga tttatcattc 6660

cctttcagcc gactggacat tgacagcatt tccaactttt caaccttgta aaaataacta 6720

attgaactat tttataacta agcatttggg caatcaatta cctctgcctg gaatgggggc 6780

aacaacacat gcaatcatgg gaaagccagg atgctgctgt ctgatcccta gccctggcat 6840

tcgtgcagaa cctcactctc atctgtgccc tgatatcctt cactctcaag tcttttccca 6900

gtgactttta aaggcaacag aatcatatag ccaataatga aagctacttg gtctacagtt 6960

gtgtggcgtt ttttatagat attttcttca tttacatttc aaatgctatc ccaaaagtcc 7020

cctataccct cccccaccct gctcccctac ccactcactc ccacttcttg gccctggctt 7080

tccccttac tggggcatat aaagtttgct agaccaaggg gcctctcttc ccaatgatgg 7140

ccaactaggc cattttctgc tacatatgca gctagagaca ccagttctgg ggttactggt 7200

tagttcatat tgttgttcta cctatggggt tgcagacccc ttcagctctt gagtactttc 7260

tctagctcct ccattgggag ccctgtgttc catcctatag atgactgtga gcatccactt 7320

ctgtatttgc caggcactgg catatgaaat agtatctgca tttggtggct gattatggga 7380

tggacccccg ggtggggcag tctctggatg gtccatcctt tcatcttagc tccaaacttt 7440

gtctctgcaa cttcttccat ggatatttta gtccctaatc tagggagaaa tgaagtatcc 7500

acaagttgat cttccttctt gattttctta tgttttagaa gttgtatctt ggatattcta 7560

ggtttctggg ctaatatcca cttatcagtg agtacatatc aagtgaattc ttttgtgatt 7620

aggttacctc actcaagatg atattctcca ctatgttcat agcagcccta tttatagtag 7680

ccagaagctg gaaagaaccc agtccctcaa cagaggaatg gatacagaaa atgtggcaca 7740

tttatgcaat ggagtaccac tcagatatta aaaacaacga atttatgaaa ttctcgggca 7800

aaaccctatc taaagaccag gaataaggaa aagatggact gcctgcctgc agctgggaga 7860

gctggggaga cctttgtgga ttctgtaata cttaggggta cggaacagct tgtggctgga 7920

taattctgag ctccagcatg tctgcccccc aaaaaacatt ctgtttttct gaaagccttt 7980

ttcttctttg cctcagtgaa gaccagacac tcccaactgc agga atg tgc tcc ctt 8036

ccc atg gca aga tac tac at gtaagtaa tcttaacgat cgctcaatca 8084

FIG. 9F

aggggcctgg agatcacatg agaagggaaa aggctgagtc aaagggacaa agctccctct 8144

agccacagaa atctcaaaca ctgaataatt gatcttcatc tttgtcaatc acaacagccc 8204

tctttcctgg tgacagaatg gaacaactgt aagagtggta ttgcttagtc cattttacag 8264

acccggaaac tcaacctcca cgaggttata caattttcct catgtcatgc aattacccaa 8324

aagcagagag tgggatcgga ctctctgttc tctaaactga tgtagctagt tcttagaaag 8384

ctcaaacaat cttgagtccc aaggacagca cctttatggt cacctggatt gatacctata 8444

tcaaaaaaaa aaaaaggtct cactagatag ccctggctac cctgaaactc tcactgtgta 8504

catttaggtg accacgaact cacagagatc tgccttccaa gtgctgggat taaagtatgt 8564

accaccacac ctgcatcttt gacaataact gagtggtatc taaattcttc cagtggctaa 8624

acagttaagt cccagttccc aaagtctgag aaaaatgcca ggtggtgaaa tctgtacaga 8684

cctttgttct taatgtacaa gtgagcctgc tttaaaaaca atacgcaagc tgtttttgct 8744

attgctaagt gttgcagaga cagaaaaggc tcccagaagt ggtaactttg gtccagaggt 8804

tctgttctca aactcattgt gagctctgaa agcaactgat gggcagctct gaaatcagct 8864

gggcaattag gctaataaca ggcataattt taatgtttca cacgcatgac agttcctccc 8924

cagctgccct agtacatact taccctccta ggcacgtcat tagacccata ggtataacca 8984

gtgactaatc aggccctggt ctaattctaa gttggcctcc tatataagtg ccactcagag 9044

tgtacctcat catggctgta gtgggcccag agtctaggga catagacttt tctattgtcc 9104

aatttctgat ttgtgaattt tctacaaaaa gaatttttt taattttaca aatcaaatca 9164

cagttactac atcttcagtt ccttcattaa ttagtgttac tatttaaaaa aataaaataa 9224

atcaagctca gaaacatcat ggatagggtt cattgtatct ccagggtacc tgagcttcaa 9284

agcaactcct cagacagcca tgaaaacatc ctcaattacc tcatgagaag acactattgt 9344

catttctgga gcctctgata atcctgagcc taggcagctt tgggatgaaa caatttctac 9404

ccttattgga acagtgtccc tctcctgtct ggaaacaatt caccaaaggc tccatgtggt 9464

tgtccagtaa ggtggtatgg ggacagaaat ggacaatgat ccctgagggc agtgatccat 9524

taaccttgcc ctcctatttc ag a atc aag gat gca cat caa aag gct ttg tac 9577

aca cgg aat ggc cag ctc ctg ctg gga gac cct gat tca gac aat tat 9625

agt cca g gtgatcttc cggtggtggg ggtgggggag tggaggggag ggtgtggggg 9681

FIG. 9G

gggctctctt ccagaagttg cttagtgtcc atctgccaca aggccttgat tctttccttc 9741

aattgtgtct ctagagacat gagaatattg tcacagtgat aaggagaaga ggtaggggca 9801

gtttcttcct gtaaaaaatg aattccattt accctgcagt ctccatacag aaacaggcca 9861

gaggggggca gacccagtaa cttctagctg agccctacct tgcttaaaac ctgccatctg 9921

tggtcccctc actgtctgaa ttgcattctg tcttacctcc cag ag aag gtc tgt atc 9978

ctt cct aac cga ggc cta gac cgc tcc aag gtc ccc atc ttc ctg ggg 10026

atg cag gga gga agt tgc tgc ctg gcg tgt gta aag aca aga gag gga 10074

cct ctc ctg cag ctg gag gtgagacacc cctcctcatt gcagtcagta 10122

ctgccactgg aacatagtga catctttgaa cccacatgtc ccctctcttg tttcccatct 10182

atctctcttt gcctccagct gagggactct agcctttggg gatgtacaga aagaacatgg 10242

cttcggaaaa ctcttcccta ttgagtcctt ctttggccaa gcctctgagg cactaagggc 10302

tgacgtccca accaaacact catttcatct cacagctgtc tccctttccc cacag gat 10360

gtg aac atc gag gac cta tac aag gga ggt gaa caa acc acc cgt ttc 10408

acc ttt ttc cag aga agc ttg gga tct gcc ttc agg ctt gag gct gct 10456

gcc tgc cct ggc tgg ttt ctc tgt ggc cca gct gag ccc cag cag cca 10504

gtg cag ctc acc aaa gag agt gaa ccc tcc acc cat act gaa ttc tac 10552

ttt gag atg agt cgg taa agagacataa ggctggggcc tcgtctagtg 10600

cccccagtct gagatcttct tgctcagcat ctctggaaag cagaataagg aagataccaa 10660

agatgtttgg gtcttaatcc ccagaatctg tgaccgtgtt acattaaatg gcaaagggat 10720

ttttttttttc cttcatggtc catttgggcc cattggaatc atctgaggcc tcatgaggag 10780

aaggaagagg tcagagggag actggggcaa actttggtac taaaagtaac aatggagaca 10840

gggaccataa gctgatgggt aacagtggtt tctagaaacc ggaaatgatg agagctctcc 10900

tgacacaggt tctggatttt tctggactga agaatggtga aataatacag ctccattatt 10960

ttaagccact gagtttgaga tcattcaatg aagctgtcat aataaaacct gtgcttcaca 11020

tacaattcaa tattggtagg caccccggtg atttcttgga aagacatcta gggattctcc 11080

tggatgctga ttccagggtc cagtggagtc cctgggttga agagatttca caacccagaa 11140

catcaggctc gactcttcta aaagtccgtc gttgcacccc ttgcctgaga gcattagcaa 11200

FIG. 9H

```
tttctatttc ataggaaatc tgtgtccctg cccctgctaa agcagggagc ctggaccgtc 11260
ctgatttagt gaggggtgag ctgctggcac ttttttgtgt caccagtgtc ttaagcagtg 11320
atggagcaca aaagatcttt actgagaaga tggccatgaa gctctggcta gacaccaaga 11380
atatgatata agcagagcta cagcacaaga tgagccaatg aggaaagcca ttcagggagg 11440
ctaagcccag cttcccaaag ggacagctaa ccctggactc aaatgaatag gggttttcct 11500
ggcagagaac ataggtcaag cattctaggt agaatcagca attcagaaag gtgtgagaga 11560
ggcatggaga gctccaggca tgtctgggct atggtgtgtc attcttgtgg caagaatcca 11620
acgtctgtgg ttaaggagtt gctgaaaatt aaaataggaa aatgggtaga gtctaattgt 11680
gaatgacttg caaaggagtt tagcccataa gtggggagct cagaggagtc atctaaggat 11740
tgcaagcagg ggccctgtga tcattgctgg accagcctag gtgctacaga gcctaccttc 11800
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gctttaccaa gggggcactg attggagaat tggaatgagg gtggttagaa tgcattcaga 12040
aaacaagggg aagaaaaatt tgattgctta aagtggaaag tcccaactta aatgttagtc 12100
agtagtttct aattacttga gtctctaatt agaggttagt tggcagtttc tggttagtta 12160
atctaagttt cattttctta ggctatgacc attctctgag tcgcatgtta gcaatgcagt 12220
aagaactcaa gacccagaat agcctctgtt aattatttta gcaatgatca ctcatttctg 12280
ttgcctccta ttgagatctg ttcccatgga ccacccaggc acatcaggcc tcctagtacc 12340
aacataataa tgattgctgc acagacaaaa tatttttttt cagtatctgg tatttgctac 12400
atttccatta gtgctggagg gaaggctaca acgaccatga aggcatggcc cctgccttct 12460
aaggacttac aatgtaatag gagccctgac attataaagt gggtcacctt gtttcaaact 12520
gagccaaact gaggctgagg gcttagatta gtggtaggtc actttccaga catgttcagt 12580
gctaagaaaa acacattctg gggttagtta gatgttttag ttcatttgat aagaagccca 12640
atgattggac tttcaacttc tggaacccat gtggtggaag agagaaccaa cttctgacca 12700
tttgggtcat ggcacatccc ctaccatcac aagaactcac caaaataaat tagaaaaatc 12760
aagaaaaact catatcctat agacctctgg tagaattagc agaacgctgc tgtggcactt 12820
```

FIG. 9I

gggatttgaa actcaaaaat ggaagaagct acttgtgacc gttcaagact ccagggaggc 12880

tcctctgaca catcccacga ctcaggctta aattccttct tctccctaga aggccacgcc 12940

atcttctcaa ccaggccaca gatgctataa ttatgtaaat gtgtgggaga ggcacacttt 13000

agatcttatc cactagt 13017

FIG. 10A

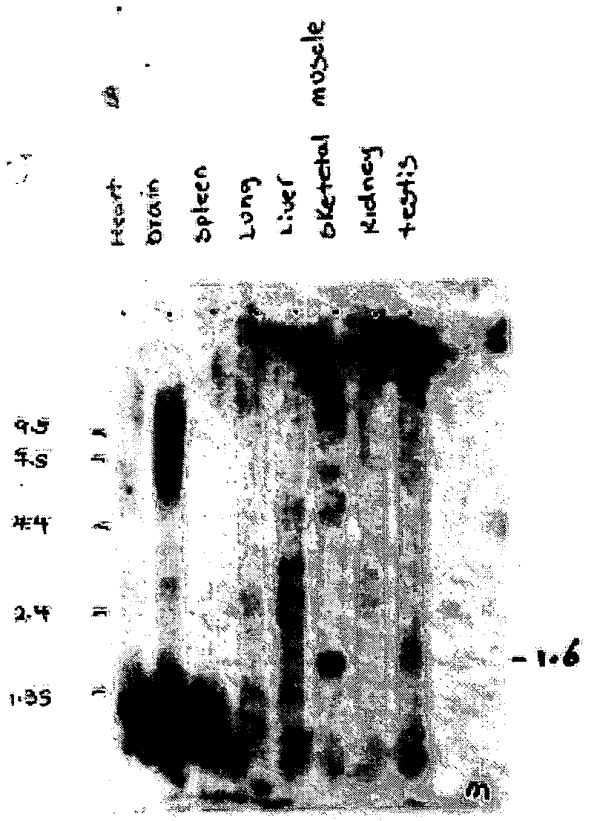


FIG. 10B

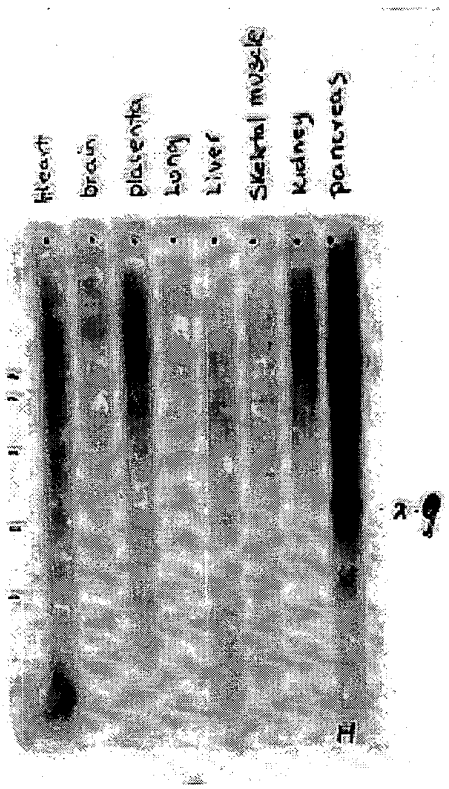


FIG. 10C

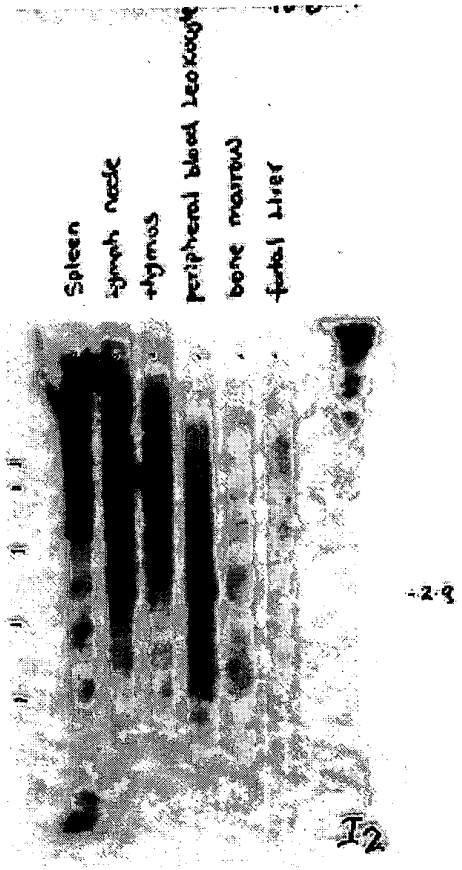


FIG. 11A

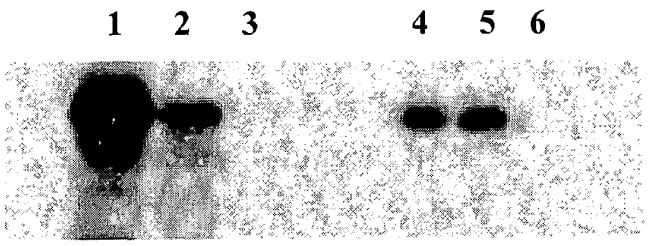


FIG. 11B

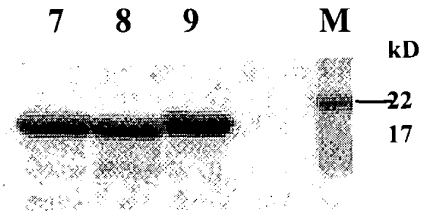


FIG. 12

Spleen

	CD4+	CD8+	CD4+ CD8+	CD3+	NK1.1+	CD3+ NK1.1+
control mice	20.18	3.72	1.67	24.07	3.06	1.4
CS329 mice	15.89	3.99	0.37	22.9	2.08	1.1
Difference:	-4.29	0.27	-1.3	-1.17	-0.98	-0.3

Bone Marrow

	CD4+	CD8+	CD4+ CD8+	CD3+	NK1.1+	CD3+ / NK1.1+
control mice	2.62	2.54	0.49	3.88	1.26	0.49
CS329 mice	2.46	2.35	0.41	4.42	1.53	0.57
Difference:	0.16	0.19	0.08	0.54	0.27	0.08

FIG. 13A

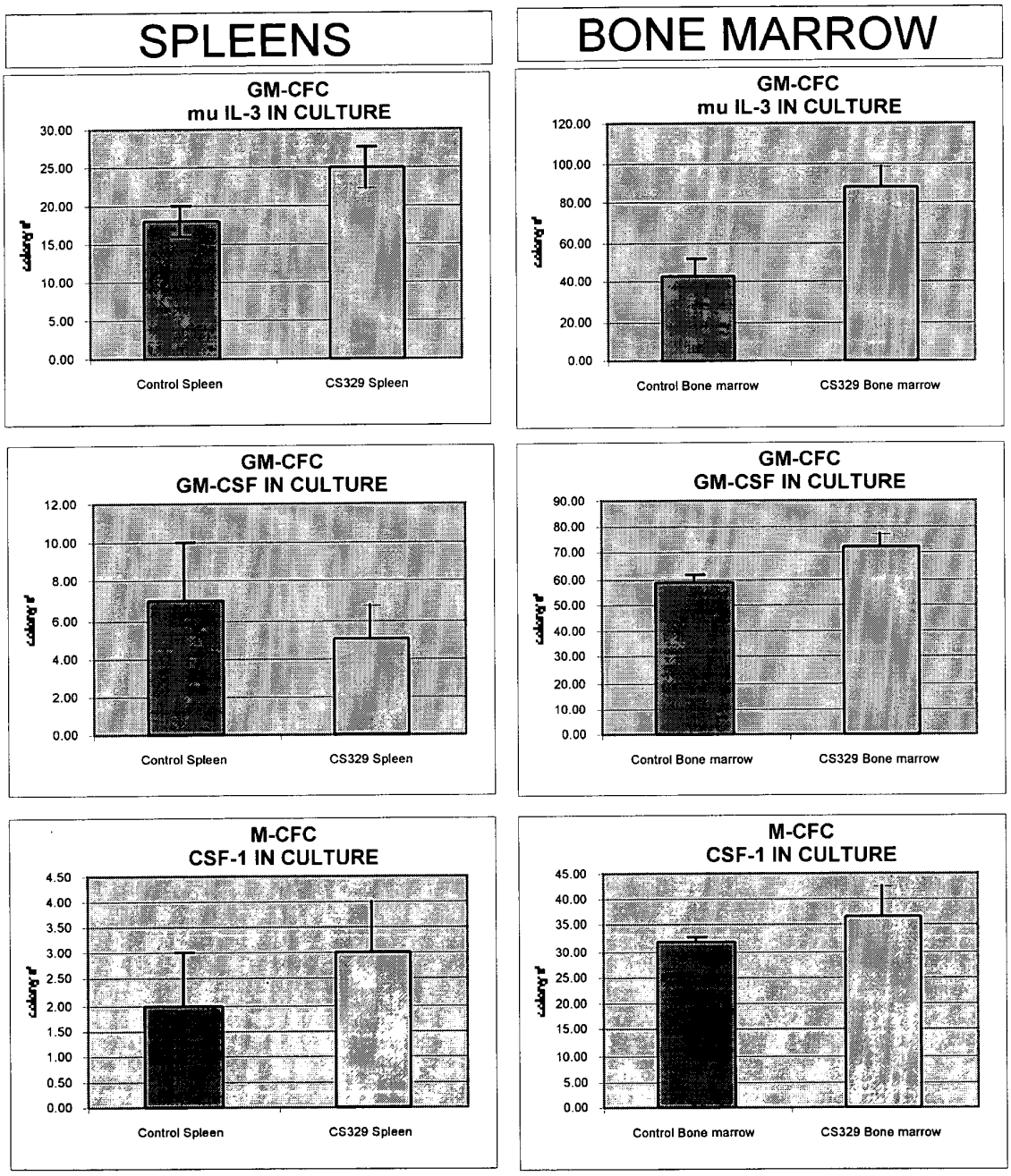

SPLEENS
BONE MARROW
GM-CFC
mu IL-3 IN CULTURE
30.00
25.00
20.00
15.00
10.00
5.00
0.00
Control Spleen
CS329 Spleen
GM-CFC
mu IL-3 IN CULTURE
120.00
100.00
80.00
60.00
40.00
20.00
0.00
Control Bone marrow
CS329 Bone marrow
GM-CFC
GM-CSF IN CULTURE
12.00
10.00
8.00
6.00
4.00
2.00
0.00
Control Spleen
CS329 Spleen
GM-CFC
GM-CSF IN CULTURE
90.00
80.00
70.00
60.00
50.00
40.00
30.00
20.00
10.00
0.00
Control Bone marrow
CS329 Bone marrow
M-CFC
CSF-1 IN CULTURE
4.50
4.00
3.50
3.00
2.50
2.00
1.50
1.00
0.50
0.00
Control Spleen
CS329 Spleen
M-CFC
CSF-1 IN CULTURE
45.00
40.00
35.00
30.00
25.00
20.00
15.00
10.00
5.00
0.00
Control Bone marrow
CS329 Bone marrow

FIG. 13B

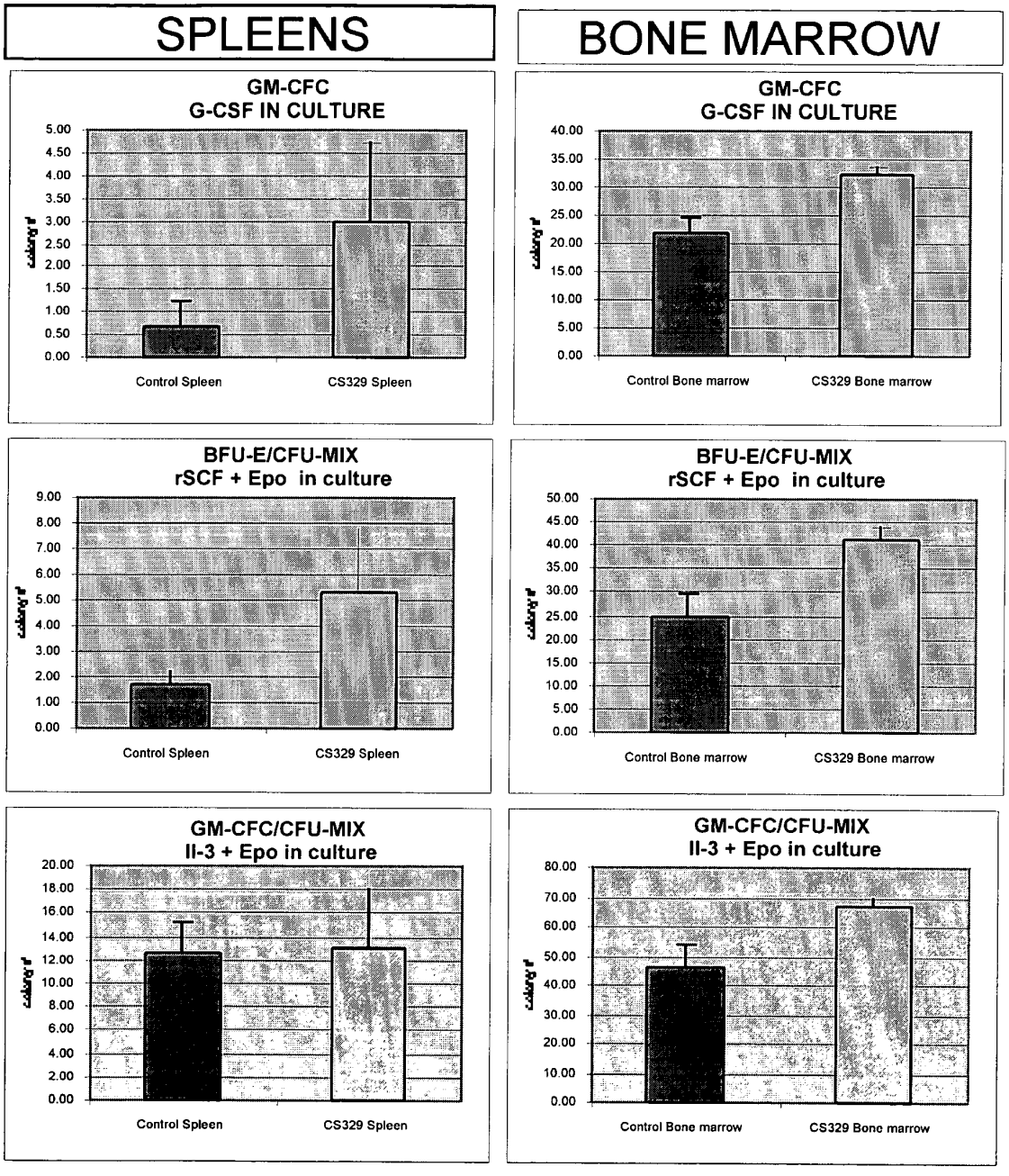

SPLEENS
BONE MARROW
GM-CFC
G-CSF IN CULTURE
5.00
4.50
4.00
3.50
3.00
2.50
2.00
1.50
1.00
0.50
0.00
Control Spleen
CS329 Spleen
GM-CFC
G-CSF IN CULTURE
40.00
35.00
30.00
25.00
20.00
15.00
10.00
5.00
0.00
Control Bone marrow
CS329 Bone marrow
BFU-E/CFU-MIX
rSCF + Epo in culture
9.00
8.00
7.00
6.00
5.00
4.00
3.00
2.00
1.00
0.00
Control Spleen
CS329 Spleen
BFU-E/CFU-MIX
rSCF + Epo in culture
50.00
45.00
40.00
35.00
30.00
25.00
20.00
15.00
10.00
5.00
0.00
Control Bone marrow
CS329 Bone marrow
GM-CFC/CFU-MIX
Il-3 + Epo in culture
20.00
18.00
16.00
14.00
12.00
10.00
8.00
6.00
4.00
2.00
0.00
Control Spleen
CS329 Spleen
GM-CFC/CFU-MIX
Il-3 + Epo in culture
80.00
70.00
60.00
50.00
40.00
30.00
20.00
10.00
0.00
Control Bone marrow
CS329 Bone marrow

FIG. 14

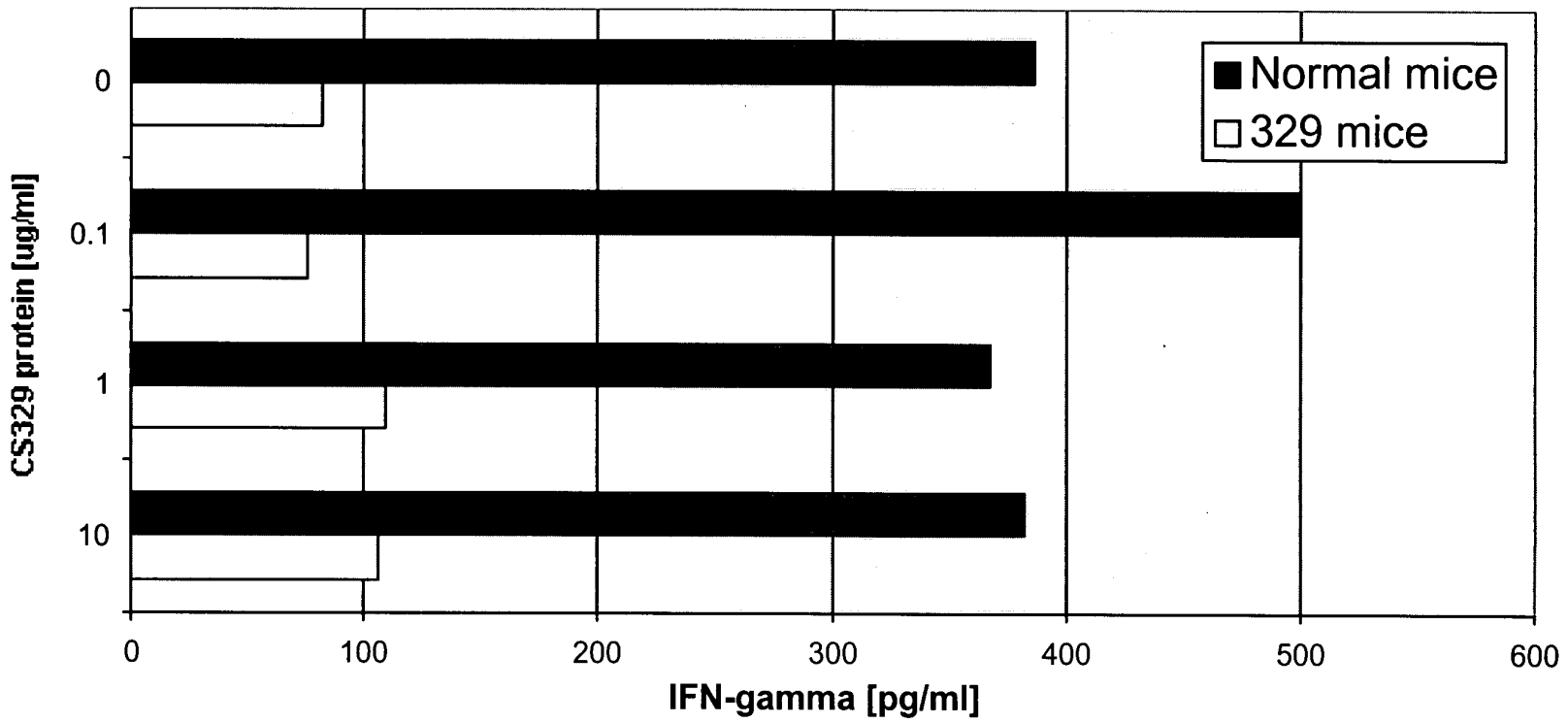
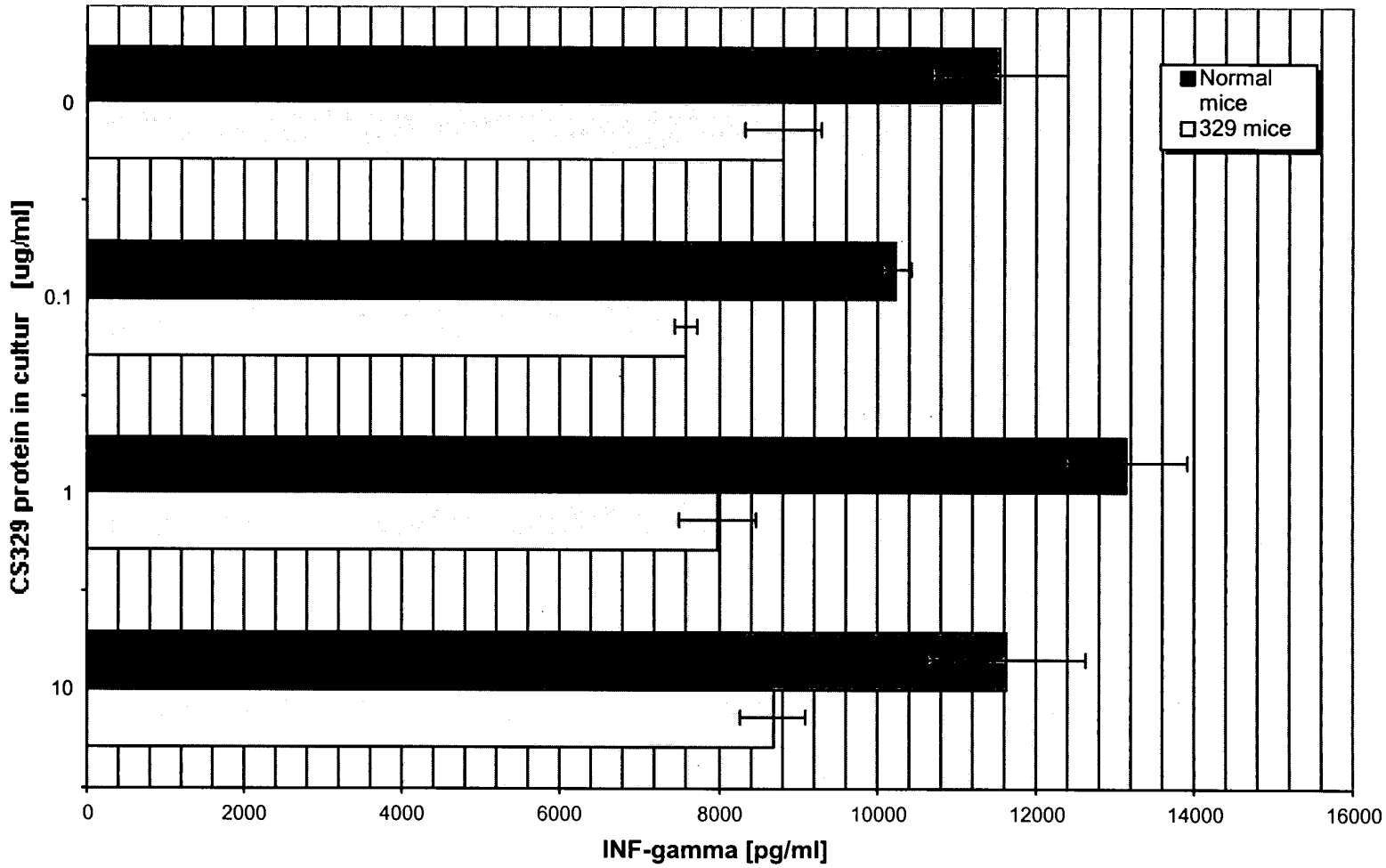

Normal mice
329 mice
CS329 protein [ug/ml]
0
0.1
1
10
0
100
200
300
400
500
600
IFN-gamma [pg/ml]

FIG. 15


Normal mice
329 mice
CS329 protein in cultur [ug/ml]
0
0.1
1
10
0
2000
4000
6000
8000
10000
12000
14000
16000
INF-gamma [pg/ml]